SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: PARANHOS-BACCALA, Glaucia
               LESENECHAL, Mylene
               JOLIVET, Michel

    (ii) TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND
        GENE ENCODING THE LATTER; THEIR APPLICATION TO THE
        DETECTION OF CHAGAS DISEASE

   (iii) NUMBER OF SEQUENCES: 13

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Oliff & Berridge
        (B) STREET: 700 South Washington Street, Suite 300
        (C) CITY: Alexandria
        (D) STATE: Virginia
        (E) COUNTRY: U.S.A.
        (F) ZIP: 22314

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/480,917
        (B) FILING DATE: 07-JUN-1995
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Berridge, William P.
        (B) REGISTRATION NUMBER: 30,024
        (C) REFERENCE/DOCKET NUMBER: WPB 36400

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 703-836-6400
        (B) TELEFAX: 703-836-2787

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3402 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AACGCTATTA TTAGAACAGT TTCTGTACTA TATTGTCATT TGGGGAGGGG GGAAAGGGGG      60

GAAGTACTTG CCGTTTTGTG TGGGTGACGA GACAACACAC ATCGAGCGGG AAGAAAAAAA     120

AAAAGGAAAT AAATTAAATT AAATTATTTG TTCTTTGAAT AGGCAAAGAA GAAGAAGAAG     180
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AAAAGGTGCG GGGGAGGGAG GAGAAAGCGA CACACACACA AAAAAAAAAA AAGGAATTGC      240

GGAAATAACA ACGCAAGGCG CGGACATGAC CGTGACGGTG GATTTGTTCA ATCATGCGAA      300

GCCGAGCAAC AATGAGGGCC GCGTGTGGTC TGTGGACGCC GCGACATTTA ACGAGGTGCC      360

TGAGGCGCAG CGTGTGCTGG CGGATTCGCA GTTTTATCTT GCCTACACCA TGAAGCGGCG      420

TCACGTGCTG CGTGTGGTGA AGCGCTCGAA CCTTTTGAAG GGCACCGTGC GGGCACACTC      480

AAAGCCCATT CATGCGGTGA AGTTTGTGAA TTACCGCAGT AACGTCGCAG CATCGGCTGG      540

GAAGGGGGAG TTCTTCGTGT GGGTTGTGAC GGATGAAACG GAGGCGAGCA ACGGCAAGCC      600

GGATCTCGCA GCCCGCCTCA CAGTGAAGGT GTACTTTAAG CTTCAGGATC CTGTCACAAT      660

TCCATGCTTT TCTTTCTTTA TCAACGCCGA GAGTCAGCGG CCTGATCTGC TTGTCCTTTA      720

CGAAACGCAG GCGGCAATTC TTGACAGCTC CTCCCTCATT GAGCGCTTTG ACGTGGAATC      780

ACTGGAGGCA ACACTACAGC GGAATTGCAC AACCCTGCGA ACCCTGACTC AACCGGTTAG      840

TGAGAACAGT TTATGCTCCG TTGGCTCTGG CGGATGGTTC ACCTTTACCA CGGAACCAAC      900

AATGGTAGCG GCATGCACAT TACGAAACCG CAGCACTCCA TCATGGGCGT GTTGCGAGGG      960

TGAGCCAGTG AAGGCATTGC ATCTCCTTGA CGCAACCGTT GAGGAAAATG TCAGTGTTCT     1020

CGTGGCCGCA TCTACAAAAG GGGTGTACCA ATGGCTCCTT ACGGGTGTAG CAGAACCAAA     1080

CTTGTTGCGC AAGTTTGTCA TTGATGGATC TATTGTCGCG ATGGAAAGCT CACGAGAAAC     1140

GTTTGCCGTG TTTGACGACA GGAAGCAGCT GGCGCTGGTC AACATGCATT CCCCTCATAA     1200

CTTTACCTGC ACACACTACA TGATGCCTTG TCAGGTACAG CGTAACGGCT TTTGCTTCAA     1260

TCGTACAGCC GACGGTAGCT GCGTCCTGGC TGACATGTCG ATTCGATTGA CGATCTTCCA     1320

TCTCCGGTCC TCCCGCAGGG AAGAACAGCA GCCAGGCCAA AAAACATCGG TAGTGGCGAC     1380

GGCGAAACCG GGGTGTGTGT CCTCGGGCAC TGACGCGGCG AGTAGCAGTC ATACCAATAC     1440

GACTTCTGCC GCTGCTGCAT CCCCTGCATC ACCCCTGTT TCAGCGCCAG CCAAGGCAGC     1500

CGCGCCTCCT GCCGCGGCGC GATCGGCTGA GCCGCACGTG GGGAGCAAGA TCATTGCTAA     1560

TCTAGTGAAT CAGCTGGGGA TTAATGTCAC CCAAAGGAGC GTCGTCAGCA CTGGAGCGCC     1620

GGCCACGACG AGGTCTACGG CGGTGACGTC CACGACTACC GCCCCGCAGC GAACAAGTCC     1680

ATACGGGCAC AATGGCCGAC CTGTGACGGC TGGATTGGTG GCAGCTAATA GTGGTGCCAG     1740

CGCGGCCTCG TCTCCCACAG CCGCGGCGAA AGCAACAGGA GAAGAAAAGG CCTCCGCGGC     1800

ATGTGAAACG AGCTCCGTGG CGATAAATGC GACACGCCCG GCGCTTCACA ACGCCTCTCT     1860

CCCGCAGGCG CCAACGGATG GCGTTTTGGC GGCAGCAGTA TACCAGTCGG AGGGCGAGGT     1920

TCATCAGTCG CTGGAGCGGC TGGAGTCCGT CATAACCAAC ACGTCTCGGG TTCTGAAGTT     1980

GCTCCCTGAC ACCATTCGAA GAGACCATGA ACAACTTCTG AATCTGGGTT TAGAGGCACA     2040
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GATGACAGAG CTGCAGCAGA GCCGTCCAAC ACCGCAAACA CAGCCGAGAG ACACAAGCTC     2100

CGCGAAATCA TCCGTGTTTG AGACGTACAC CCTTGTTCTC ATTGCGGATT CCCTCTCTCG     2160

CAACATCACG AAGGGGGTGA AGCGTGGTGT GAACGAGGCC ATTATGTTGC ATCTCGACCA     2220

TGAGGTGCGG CACGCCATAG GGAACCGGCT TCGGCAAACA CAAAAGAACA TCATCAAGAG     2280

CCGCCTCGAT GAAGCGTTGA AGGAAAGCAC TACACAGTTT ACGGCTCAAT TGACGCAAAC     2340

GGTGGAGAAT CTGGTGAAGC GCGAGCTTGC CGAGGTGCTT GGTAGCATCA ACGGCTCCCT     2400

CACTTCTCTC GTGAAGGAAA ATGCCTCATT ACAGAAAGAG TTGAATTCCA TAATGTCTAG     2460

TGGGGTGTTG GATGAAATGC GTCGTATGCG GGAAGAGCTG TGCACATTGC GAGAGTCCGT     2520

TGCGAAGCGG AAGGCAACAA TGCCAGATTC TTCTCTTCAC GCCACGAGCT CCTTTCAAGG     2580

AAGAAGGTCT GCGCCCGAGA CAATTCTTGC AACCGCGTTA TCGATGGTGC GAGAGCAGCA     2640

GATACCGTCAG GGACTGGAAT ACATGTTGAT GGCTCAGCAG CCCTCTCTCC TCCTGCGGTT     2700

CCTCAGCATA CTTACAAGGG AAAACGAAAA CGCCTACTCG GAACTTATTG AAAATGTAGA     2760

GACGCCGAAT GACGTGTGGT GTTCGGTTCT GTTGCAACTC ATAGAGGCCG CGGCGACCGA     2820

GGCTGAGAAG GAGGTGGTTG TTGGCGTCGC CATTGATATT CTCTCCGAGC GCGATCAAAT     2880

TGCTCAGAAC GGCGCACTCG GCTCGAAACT CACCACCGCC ATGCGAGCCT TTGAGCGACA     2940

GGCAAGGTCG GAGACAACGA GCAGGTCATT CTTGCAATGC CTGAAGAACC TGGAAAAGCT     3000

TCTGCAATCA TGATAATAAA AAGAACTCAA CGAATACAGT TGTTGATTAT TAAGGAAGGG     3060

AAAAGAGAGA AAGAGAGAGA GAGAGAGAGA AATGTAATGG GCGTTTAGTT ACGGTAGAAA     3120

GAAAACGTGT GGATAAGAAG GAGGGGTTTT GTGTGCGACC AGGAATTACT GGGGAACGCT     3180

GCTACACGGC GGAATCGACC ATTTTATTAT TATTATTATT GTCTTTAGTA TTATGTTTTT     3240

TCTTGTGTGT GTGTGTGTGT GTTTGTGTGT GTGCGGTTAT TTTGTATCCG TTTGCTCCCG     3300

CCCCTGCCCC CCATCACCCG AGGAGAAAGT AGAATAAGAC ACATACGATT GTTGTTTTTG     3360

TTATCCTTAA AAGGAAGAGA GACCAAAAAA AAAAAAAAAA AA                        3402
```

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 915 amino acids
             (B) TYPE: amino acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: other nucleic acid
             (A) DESCRIPTION: /desc = "protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Thr Val Thr Val Asp Leu Phe Asn His Ala Lys Pro Ser Asn Asn
1               5                   10                  15

Glu Gly Arg Val Trp Ser Val Asp Ala Ala Thr Phe Asn Glu Val Pro
            20                  25                  30

Glu Ala Gln Arg Val Leu Ala Asp Ser Gln Phe Tyr Leu Ala Tyr Thr
            35                  40                  45

Met Lys Arg Arg His Val Leu Arg Val Val Lys Arg Ser Asn Leu Leu
        50              55                  60

Lys Gly Thr Val Arg Ala His Ser Lys Pro Ile His Ala Val Lys Phe
65                  70                  75                  80

Val Asn Tyr Arg Ser Asn Val Ala Ala Ser Ala Gly Lys Gly Glu Phe
                85                  90                  95

Phe Val Trp Val Val Thr Asp Glu Thr Asp Ala Ser Asn Gly Lys Pro
            100                 105                 110

Asp Leu Ala Ala Arg Leu Thr Val Lys Val Tyr Phe Lys Leu Gln Asp
        115                 120                 125

Pro Val Thr Ile Pro Cys Phe Ser Phe Phe Ile Asn Ala Glu Ser Gln
        130                 135                 140

Arg Pro Asp Leu Leu Val Leu Tyr Glu Thr Gln Ala Ala Ile Leu Asp
145                 150                 155                 160

Ser Ser Ser Leu Ile Glu Arg Phe Asp Val Glu Ser Leu Glu Ala Thr
                165                 170                 175

Leu Gln Arg Asn Cys Thr Thr Leu Arg Thr Leu Thr Gln Pro Val Ser
            180                 185                 190

Glu Asn Ser Leu Cys Ser Val Gly Ser Gly Gly Trp Phe Thr Phe Thr
            195                 200                 205

Thr Glu Pro Thr Met Val Ala Ala Cys Thr Leu Arg Asn Arg Ser Thr
    210                 215                 220

Pro Ser Trp Ala Cys Cys Glu Gly Glu Pro Val Lys Ala Leu His Leu
225                 230                 235                 240

Leu Asp Ala Thr Val Glu Glu Asn Val Ser Val Leu Val Ala Ala Ser
            245                 250                 255

Thr Lys Gly Val Tyr Gln Trp Leu Leu Thr Gly Val Ala Glu Pro Asn
            260                 265                 270

Leu Leu Arg Lys Phe Val Ile Asp Gly Ser Ile Val Ala Met Glu Ser
        275                 280                 285

Ser Arg Glu Thr Phe Ala Val Phe Asp Asp Arg Lys Gln Leu Ala Leu
        290                 295                 300

Val Asn Met His Ser Pro His Asn Phe Thr Cys Thr His Tyr Met Met
305                 310                 315                 320
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Pro Cys Gln Val Gln Arg Asn Gly Phe Cys Phe Asn Arg Thr Ala Asp
            325                 330                 335

Gly Ser Cys Val Leu Ala Asp Met Ser Asn Arg Leu Thr Ile Phe His
            340             345                 350

Leu Arg Cys Ser Arg Arg Glu Glu Gln Gln Pro Gly Gln Lys Thr Ser
            355             360                 365

Val Val Ala Thr Ala Lys Pro Gly Cys Val Ser Ser Gly Thr Asp Ala
    370             375             380

Ala Ser Ser Ser His Thr Asn Thr Thr Ser Ala Ala Ala Ala Ser Pro
385             390                 395                 400

Ala Ser Pro Pro Val Ser Ala Pro Ala Lys Ala Ala Ala Pro Pro Ala
            405                 410                 415

Ala Ala Arg Ser Ala Glu Pro His Val Gly Ser Lys Ile Ile Ala Asn
            420                 425                 430         .

Leu Val Asn Gln Leu Gly Ile Asn Val Thr Gln Arg Ser Val Val Ser
            435             440                 445

Thr Gly Ala Pro Ala Thr Thr Arg Ser Thr Ala Val Thr Ser Thr Thr
    450             455                 460

Thr Ala Pro Gln Arg Thr Ser Pro Tyr Gly His Asn Gly Arg Pro Val
465             470             475                 480

Thr Ala Gly Leu Val Ala Ala Asn Ser Gly Ala Ser Ala Ala Ser Ser
            485             490                 495

Pro Thr Ala Ala Ala Lys Pro Thr Gly Glu Glu Lys Ala Ser Ala Ala
        500             505                 510

Cys Glu Thr Ser Ser Val Ala Ile Asn Ala Thr Arg Pro Ala Leu His
    515             520             525

Asn Ala Ser Leu Pro Gln Ala Pro Thr Asp Gly Val Leu Ala Ala Ala
    530             535             540

Val Tyr Gln Ser Glu Gly Glu Val His Gln Ser Leu Glu Arg Leu Glu
545             550             555             560

Ser Val Ile Thr Asn Thr Ser Arg Val Leu Lys Leu Leu Pro Asp Thr
            565             570                 575

Ile Arg Arg Asp His Glu Gln Leu Leu Asn Leu Gly Leu Glu Ala Gln
            580             585                 590

Met Thr Glu Leu Gln Gln Ser Arg Pro Thr Pro Gln Thr Gln Pro Arg
            595             600                 605

Asp Thr Ser Ser Ala Lys Ser Ser Val Phe Glu Thr Tyr Thr Leu Val
    610             615             620

Leu Ile Ala Asp Ser Leu Ser Arg Asn Ile Thr Lys Gly Val Lys Arg
625             630             635                 640

Gly Val Asn Glu Ala Ile Met Leu His Leu Asp His Glu Val Arg His
        645                 650                 655
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Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser
        660                 665             670

Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln
        675             680             685

Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val
690             695             700

Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala
705             710             715             720

Ser Leu Lys Lys Glu Leu Asn Ser Ile Met Ser Ser Gly Val Leu Asp
            725             730             735

Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val
        740             745             750

Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser
        755             760             765

Ser Phe Gln Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala
    770             775             780

Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met
785             790             795             800

Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu
            805             810             815

Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu
            820             825             830

Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala
        835             840             845

Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp
    850             855             860

Ile Leu Ser Glu Arg Asp Gln Ile Ala Gln Asn Gly Ala Leu Gly Ser
865             870             875             880

Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu
            885             890             895

Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu
        900             905             910

Leu Gln Ser
    915
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "phage DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTGGCGACG ACTCCTGGAG CCCG   24

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "phage DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACCAG ACCAACTGGT AATG   24

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGGGCACTG ACGCGGCG   18

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "phage lambda gt10 DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTATGAGTA TTTCTTCCAG GGTA   24

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACGCTATTA TTAGAACAGT T   21

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCAGCAGCG GCAGAAGT   18

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCCGACGG TAGCTGCGTC CT   22

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACATAATGGC CTCGTTCACA C   21

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 34 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GACTCGCTGC AGATCGATTT TTTTTTTTTT TTTT   34

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAAGAGACC ATGAACAACT T   21

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "DNA"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACTCGCTGC AGATCGAT   18